AMENDMENT TO THE CLAIMS

This listing of claims will replace all prior versions and listings of claims in the application.

1. (Currently amended) Method for detecting the presence of a bacterial pathogen in a clinical sample comprising the steps of:

at least partially isolating nucleic acid from said sample, wherein said nucleic acid is selected from a group consisting of total nucleic acid, total DNA and total RNA,

quantifying an amount of nucleic acid from said sample comprising a 16S/23S rDNA spacer region which is specific for said bacterial pathogen by means of Polymerase Chain Reaction monitored in real time by means of multiple hybridization probes, wherein said multiple hybridization probes comprise SEQ ID NOS: 3, 4, 5, 8, 9, 10, 11, 12 and 13,

monitoring temperature dependence of hybridization of said multiple hybridization probes to said 16S/23S spacer region, wherein said monitoring temperature dependence of hybridization is effective to detect the presence of a group of predetermined species of said bacterial pathogen, and

performing at least two of:

a) determining whether said amount of nucleic acid from said sample comprising the 16S/23S rDNA spacer region is above a first predetermined cut off value,
b) determining whether said amount of nucleic acid from said sample comprising the 16S/23S rDNA spacer region is less than a second predetermined cut off value which is less than said first predetermined cut off value, and
c) determining whether said amount of nucleic acid from said sample comprising the 16S/23S rDNA spacer region is less than said first predetermined cut off value and above said second predetermined cut off value,

wherein said amount of nucleic acid from said sample comprising the 16S/23S rDNA spacer region is indicative of the presence of said bacterial pathogen if said amount of nucleic acid

from said sample comprising the 16S/23S rDNA spacer region is above said first predetermined cut off value,

wherein said amount of nucleic acid from said sample comprising the 16S/23S rDNA spacer region is indicative of the absence of said bacterial pathogen if said amount of nucleic acid from said sample comprising the 16S/23S rDNA spacer region is less than said second predetermined cut off value, or

wherein said bacterial pathogen is not confirmed nor excluded if said amount of nucleic acid from said sample comprising the 16S/23S rDNA spacer region is above said second predetermined cut off value but is less than said first predetermined cut off value.

2-4 (Canceled)

5. (Previously amended) Method according to claim 1, wherein said clinical sample is whole blood.

6-8. (Canceled)